

NEW SHEET

(3) Sequence Description: Figure 11A

1 ATGTCCCCTATACTAGTTATTGGAAAATTAAGGCCTTGCAACCC  
5 MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro 16

49 ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTG  
ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu 32

10 97 TATGAGCGCGATGAAGGTGATAAAATGGCGAACAAAAAGTTGAATTG  
TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu 48

15 145 GGTTTGGAGTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA  
GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys 64

193 TTAACACAGTCTATGCCCATCACGTTATATAGCTGACAAGCACAAC  
LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn 80

20 241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTCAATGCTTGAA  
MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu 96

289 GGAGCGGGTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGT  
GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer 112

25 337 AAAGACTTTGAAACTCTCAAAGTTGATTTCTTAGCAAGCTACCTGAA  
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

30 385 ATGCTGAAAATGTCGAAGATCGTTATGTCATAAAACATATTTAAAT  
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT  
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

35 481 GTTGTGTTATACATGGACCCAATGTGCCTGGATGCGTTCCAAAATTA  
ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu 176

NEW SHEET

(3) Sequence Description (continued): Figure 11B

529    GTTTGTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC  
      ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr 192

5      577    TTGAAATCCAGCAAGTATATAGCATGGCCTTGCAAGGGCTGGCAAGGCC  
         LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla 208

10     625    ACGTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGT  
         ThrPheGlyGlyAspHisProProLysSerAspLeuValProArg 224

10     673    GGATCCATGAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAAC  
         GlySerMetSerThrIleProLysProGlnArgLysThrLysArgAsn 240

721    ACCAACCGTCGCCACAGGAATTCATCGTGAUTGACTGA  
         ThrAsnArgArgProGlnGluPheIleValThrAspEnd 252

NEW SHEET

(4) Sequence Description: Figure 12 A

1	ATGTCCCCCTATACTAGGTATTGGAAAATTAAGGCCTTGTGCAACCC MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro	16
5	ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTG ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu	32
97	TATGAGCGCGATGAAGGTGATAAAATGGCGAACAAAAAGTTGAATTG TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu	48
10	GGTTTGGAGTTCCCAATCTCCTTATTATATTGATGGTGATGTTAAA GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys	64
15	TTAACACAGTCTATGCCCATCACGTTATATAGCTGACAAGCACAAAC LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn	80
241	ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTCAATGCTTGAA MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu	96
20	GGAGCGGTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGT GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer	112

NEW SHEET

(4) Sequence Description (continued): Figure 12B

337 AAAGACTTGAACCTCTCAAAGTTGATTTCTTAGCAAGCTACCTGAA  
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

5 385 ATGCTGAAAATGTTCGAACGATCGTTATGTCATAAACATATTAAAT  
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTGAT  
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

10 481 GTTGTAAACATGGACCCATGTCATGGATGCGTCCAAAATTAA  
ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu 176

15 529 GTTTGTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC  
ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr 192

577 TTGAAATCCAGCAAGTATATAGCATGGCCTTGCAAGGCTGGCAAGCC  
LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla 208

20 625 ACGTTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCCGCT  
ThrPheGlyGlyAspHisProProLysSerAspLeuValProArg 224

673 GGATCCGACGTCAAGTTCCCGGGTGGCGGTCAAGATCGTTGGTGGAGTT  
GlySerAspValLysPheProGlyGlyGlyGlnIleValGlyGlyVal 240

25 721 TACTTGTTGCCGCGCAGGGAATTCATCGTGACTGACTGA  
TyrLeuLeuProArgArgGluPheIleValThrAspEnd 252

NEW SHEET

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(6) Sequence Description: Figure 13A

1 ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC  
MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro 16

10 49 ACTCGACTTCTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTG  
ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu 32

97 TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTGAATTG  
TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu 48

15 145 GGTGGAGTTCCCAATCTCCTTATTATATTGATGGTGATGTTAAA  
GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys 64

20 193 TTAACACAGTCTATGCCCATCACGTTATAGCTGACAAGCACAAAC  
LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn 80

241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTCATGCTTGAA  
MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu 96

25 289 GGAGCGGTTTGGATATTAGATAACGGTGTTCGAGAATTGCATATAGT  
GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer 112

30 337 AAAGACTTTGAAACTCTCAAAGTTGATTTCTTAGCAAGCTACCTGAA  
LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu 128

385 ATGCTGAAAATGTCGAAGATCGTTATGTCATAAACATATTAAAT  
MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn 144

35 433 GGTGATCATGTAACCCATCCTGACTTCATGTTGATGACGCTCTTGAT  
GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp 160

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(6) Sequence Description (continued): Figure 13B

481	GTTGTTTATACATGGACCCAATGTGCCTGGATGCGTTCCAAAATTA ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu	176
5	529 GTTTGTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr	192
10	577 TTGAAATCCAGCAAGTATATAGCATGCCCTTGCAGGGCTGGCAAGCC LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla	208
15	625 ACGTTGGTGGTGGCGACCATCCTCCAAATCGGATCTGGTTCCCGCT ThrPheGlyGlyAspHisProProLysSerAspLeuValProArg	224
20	673 GGATCCAGCACGATTCCAAACCTCAAAGAAAAACCAAACGTAACACC GlySerSerThrIleProLysProGlnArgLysThrLysArgAsnThr	240
	721 AACCGTCGCCACAGGACGTCAAGTTCCCGGTGGCGGTCAAGATCGTT AsnArgArgProGlnAspValLysPheProGlyGlyGlnIleVal	256
	769 GGTGGAGTTACTTGTGCCGCGCAGGAAATTCACTCGTGAUTGACTGA GlyGlyValTyrLeuLeuProArgArgGluPheIleValThrAspEnd	271

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(7) Sequence Description: Figure 14

5'-GATCCATGAGCACGATTCCAAACCTCAAAGAAAAACCAAACGTAACACCAACC GT CGC  
CCACAGG-3'

5 (8) Sequence Description: Figure 15

5'-AATT CCT GT GGG CG AC GG TT GG GT TAC GTT GG TTT CT T GAG GTT GGG AAT CGT  
GCT CAT G-3'

(9) Sequence Description: Figure 16

5'-GATCCGACGTCAAGTTCCC GG GT GG CG GT CAG AT CGT TGG TGG AG T TACT GTT GCC G  
CGCAGGG-3'

10 (10) Sequence Description: Figure 17

5'-AATT CCT GT GCG GGA ACA AGT AAA ACT CCAC CAAC GAT CT GAC CG CC ACC CG GG AACT T  
GAC GT CG-3'

15 (13) Sequence Description: Figure 18

5'-GA ATT CCT TAC CT GCG CGG CA ACA AGT AAA ACT C-3'

20 (14) Sequence Description: Figure 19

5'-GCT GG AT CCAG CAC GATT CCC AAAC CT CAA AG-3'